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## STIC Biotechnology Systems Branch

### CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 10/593,426  
Filing Date: 9/19/06  
Date Processed by STIC: 9/27/06

STIC Contact: Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221

#### Nature of CRF Problem:

- ☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)
- ☐ Blank (no files on CRF) (see attached)
- ☐ Empty file (filename present, but no bytes in file) (see attached)
- ☐ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached)
- ☐ Not saved in ASCII text
- ☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should only be the Sequence Listing.
- ☐ Did not contain a Sequence Listing. (see attached sample)
- ☒ Other: Alpha numeric loadings in sequence.

PLEASE USE THE CHECKER VERSION 4.3.1 PROGRAM TO REDUCE ERRORS.  
SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,  
Alexandria, VA 22314

Revised 08/30/05

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	10/593,426
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	

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(Sample of submitted file)

PAGE 1

SEQUENCE LISTING

<110> PAPES, Fabio  
GERHARDT, Isabel Rodrigues  
ARRUDA, Paulo

<120> CAMBIUM/XYLEM-PREFERRED PROMOTERS AND USES THEREOF

<130> ALEL 202.1 PCT

<140>  
<141>

<150> US 60/560,227

<151> 2004-04-06

<160> 41

<170> PatentIn version 3.2

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 1

<211> LENGTH: 3035

<212> TYPE: DNA

<213> ORGANISM: Populus sp.

<220> FEATURES:

<221> NAME/KEY: promoter

<222> LOCATION: (1)...(3035)

<223> OTHER INFORMATION: Sucrose synthase (SUSY) promoter

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980

pls see item #1 on error  
Summary sheet.

pls delete

pls delete,  
invalid  
numeric  
identifiers.

pls do not insert  
Alpha numeric headings  
in sequence.

These types  
of errors  
are seen  
globally  
throughout  
the sequence.

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Page 2

tcatctctct tgtctattag cttgtccccc cgteccgactg ctttctgtat ttattctggc attaaagctta  
 1050  
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 2940  
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SAMP  
ERRORSSee  
item

# 1

on error

Summary  
Sheet

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PAGE 3

3010

tegtttctc ttaaggagct atggc

3035

← Same  
error

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page 4

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 13

<211> LENGTH 31

<212> TYPE DNA

<213> ORGANISM/SOURCE synthetic

<221> NAME/KEY primer/oligonucleotide

<400> SEQUENCE: 13

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pls delete, Invalid numeric identifier

Invalid response

insert on line <223>

delete

pls use lower case

FYI:

<213> responses  
CAN ONLY be  
either  
Artificial/  
Unknown or  
Genus/Species,

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

see item  
# 10 on  
error  
summary  
sheet.